In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 1, lines 18-34 and replace it with the following paragraph:

Before the advent of adefovir (ADV) therapy, lamivudine and interferon were the only two approved therapies for the treatment of chronic hepatitis B virus infection. Interferon therapy is associated with serious side effects including flu-like symptoms, fever, and depression. Long-term lamivudine therapy is limited by the high incidence and rapid onset of resistance that occurred in 24% of patients at one year and 70% of patients after four years of therapy [1]. Lamivudine resistance is predominately associated with mutations (rtM204V or rtM204I) in the YMDD motif **(SEQ ID NO: 1)** in the C domain of the HBV polymerase (reverse transcriptase, or "rt"). The consensus nomenclature of HBV polymerase mutations is used throughout this report [2]. The rtL180M and rtV173L mutations in the B domain of HBV polymerase were also frequently observed in conjunction with the YMDD **(SEQ ID NO: 1)** mutations in lamivudine-resistant HBV. The B domain mutations did not confer significant resistance to lamivudine on their own. Instead, these mutations appeared to enhance replication fitness of the YMDD **(SEQ ID NO: 1)** mutant HBV [3]. Other HBV polymerase mutations were reported at much lower frequencies in patients receiving lamivudine. These low frequency mutations have not been established as lamivudine resistance mutations.

Please delete the paragraph on page 2, line 29 to page 3, line 7, and replace it with the following paragraph:

We have now identified five HBV rt and HBsAg mutations associated with adefovir resistance: rtN236T, rtA181V, rtA181T, surface antigen ("sAg") L173F and sAg which is terminated immediately N-terminal to residue L172 (hereafter "sL172trunc"). The sAg and rt position 181 mutations are related in that the open reading frame for rt and sAg overlap in part. The rtA181V and rtA181T mutants correspond respectively to the sL173F and

sL172trunc mutants (the latter resulting from substitution of a stop codon into the sAg reading frame). The HbsAg sequence before the introduced stop codon is SVRFS **(SEQ ID NO: 2)**, with the C-terminal serine residue being at sAg position 171.

Please delete the paragraph on page 16, lines 8-23, and replace it with the following paragraph:

All conserved site substitutions were evaluated for their effects on adefovir susceptibility using a novel approach to generate full-length patient-derived HBV clones. Briefly, viral DNA was extracted from patient serum and whole HBV genomes (3.2 kilobase) were PCR amplified using primers P1 (5'-CCG GAA AGC TTG AGC TCT TCT TTT TCA CCT CTG CCT AAT CA-3')**(SEQ ID NO: 3)** and P2 (5'-CCG GAA AGC TTG AGC TCT TCA AAA AGT TGC ATG GTG CTG G-3') **(SEQ ID NO: 4)**. Full-length viral genomes were cloned into the lethal selection vector $pCAP^S$ at a Mlu NI site through blunt-end ligation (PCR Cloning Kit, Roche) and then subcloned into plasmid pHY106, a pBluescript KS (+)-derived plasmid containing a CMV promoter and the minimal 5' and 3' HBV sequence necessary (approximately 180 total bases) for viral replication after the insertion of a genome-length clinical HBV isolate. Drug susceptibility of patient-derived clones was analyzed by transient transfection into HepG2 cells. Transfected cells were treated with various concentrations of adefovir or lamivudine for 7 days and the amounts of intracellular replicating virus DNA were then quantified by Southern blotting to determine adefovir sensitivity.

Please delete the paragraph on page 16, lines 6-9, and replace it with the following paragraph:

The nucleotide coding sequences for the rtN236T, rtA181V or T mutations and the surrounding sequences from patients who developed these mutations are summarized in the following table (Table 3a**; see SEQ ID NOS 5-24, respectively in order of appearance**). The corresponding changes in enzyme restriction sites are also listed in the table.